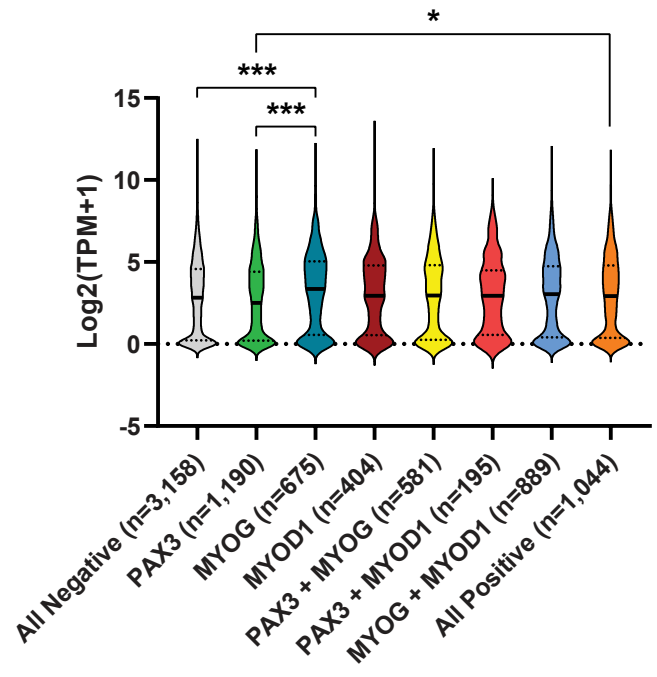


(A)

Cluster:	Transcription Factors Bound	1 <sup>st</sup> motif % (positive/total sites)	2 <sup>nd</sup> motif % (positive/total sites)
Cluster 1	FOXF1 alone		
		Sites: <b>81.5%</b> (4834/5931)	Sites: <b>19.1%</b> (1135/5931)
		E-value: 1.6E-1442	E-value: 1.1E-93
Cluster 2	FOXF1 PAX3/FOXO1		
		Sites: <b>73.6%</b> (1536/2087)	Sites: <b>18.1%</b> (378/2087)
		E-value: 1.5E-410	E-value: 1.9E-67
Cluster 3	FOXF1 MYOD1		
		Sites: <b>92.5%</b> (433/468)	Sites: <b>20.7%</b> (97/468)
		E-value: 9.5E-444	E-value: 5.4E-52
Cluster 4	FOXF1 MYOG		
		Sites: <b>83.1%</b> (709/853)	Sites: <b>22.3%</b> (190/853)
		E-value: 4.3E-571	E-value: 2.0E-112
Cluster 5	FOXF1 PAX3/FOXO1 MYOD1		
		Sites: <b>89.6%</b> (207/231)	Sites: <b>29.4%</b> (68/231)
		E-value: 1.2E-126	E-value: 1.7E-15
Cluster 6	FOXF1 PAX3/FOXO1 MYOG		
		Sites: <b>55.3%</b> (472/853)	Sites: <b>36.5%</b> (311/853)
		E-value: 8.9e-173	E-value: 5.7e-240
Cluster 7	FOXF1 MYOD1 MYOG		
		Sites: <b>90.7%</b> (1007/1110)	Sites: <b>42.1%</b> (467/1110)
		E-value: 1.5E-802	E-value: 1.2E-280
Cluster 8	FOXF1 PAX3/FOXO1 MYOD1 MYOG		
		Sites: <b>59.3%</b> (957/1615)	Sites: <b>43.6%</b> (704/1615)
		E-value: 2.7E-367	E-value: 2.1E-340

(B)



(C)

